

Title: US-10-825-378-31
 Perfect score: 1317
 Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:27:24 ; Search time 50 Seconds
 (without alignments)
 411.394 Million cell updates/sec

Title: US-10-825-378-31
 Perfect score: 1317
 Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:39:25 ; Search time 177 Seconds
(without alignments)
615.003 Million cell updates/sec

Title: US-10-825-378-31
Perfect score: 1317
Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:39:50 ; Search time 22 Seconds
(without alignments)
244.032 Million cell updates/sec

Title: US-10-825-378-31
Perfect score: 1317
Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:22:25 ; Search time 41 Seconds
(without alignments)
551.486 Million cell updates/sec

Title: US-10-825-378-31
Perfect score: 1317
Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:18:55 ; Search time 295 Seconds
(without alignments)
736.877 Million cell updates/sec

Title: US-10-825-378-31
Perfect score: 1317
Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000